



SEQUENCE LISTING

<110> Kadler, Karl
Bulleid, Neil
Ashcroft, Gillian

<120> Modified Peptides and Their Uses

<130> 17695-0002

<140> US 10/554,068

<141> 2005-10-21

<150> PCT/GB2004/00171

<151> 2004-04-21

<150> GB 0309064.4

<151> 2003-04-22

<160> 28

<170> PatentIn version 3.3

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<223> DNA molecule based on procollagen type III N-propeptide.
Sequence prior to N100 replaced with the sequence for the G123
domains of the alpha3 chain of laminin-5 whilst retaining the
collagen III signal sequence.

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 <213> Artificial Sequence

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 <223> Sequence of the modified pro-alpha chain
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His Pro Thr Ile Ile Leu Ala Thr Ser Leu Ser Leu Phe Leu Gln Arg
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Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr
 35 40 45

Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val
 50 55 60

Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu
 65 70 75 80

Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val
 85 90 95

Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn
 100 105 110

Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr
 115 120 125

Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu
 130 135 140

Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro
 145 150 155 160

Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp
 165 170 175

Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn
 180 185 190

Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser
 195 200 205

Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln
 210 215 220

Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val
 225 230 235 240

Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser

245	250	255
Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser		
260	265	270
Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg		
275	280	285
Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp		
290	295	300
Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp		
305	310	315
Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg		
325	330	335
Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys		
340	345	350
Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys		
355	360	365
Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg		
370	375	380
Gly Gly Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr Asp His		
385	390	395
Leu Gln Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Ile Leu		
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Gly Tyr Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile Phe Lys		
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Ser Pro Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser Val Ile		
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Ser Asp Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu Leu Arg		
465	470	475
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Asn Ser Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser Leu Arg
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Leu Gly Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe Val Gln
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Arg Leu Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn Ser Leu
 515 520 525

Lys Arg Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe
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Leu Met Leu Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys Thr Phe
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Val Lys Val Trp Gln Asp Ala Asn Gly Gln Gly Pro Gln Gly Pro Lys
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 595 600 605

Ile Pro Gly Gln Pro Gly Ser Pro Gly Ser Pro Gly Pro Pro Gly Ile
 610 615 620

Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp
 625 630 635 640

Ser Tyr Asp Val Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr
 645 650 655

Pro Gly Pro Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Thr Ser
 660 665 670

Gly His Pro Gly Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly
 675 680 685

Glu Pro Gly Gln Ala Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly Ala
 690 695 700

Ile Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro
 705 710 715 720

Gly Arg Pro Gly Glu Arg Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly
 725 730 735

Pro Ala Gly Ile Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe
 740 745 750

Asp Gly Arg Asn Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys
 755 760 765

Gly Glu Asn Gly Leu Pro Gly Glu Asn Gly Ala Pro Gly Pro Met Gly
 770 775 780

Pro Arg Gly Ala Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala
 785 790 795 800

Ala Gly Ala Arg Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro
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Gly Pro Pro Gly Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser Pro Gly
 820 825 830

Ala Lys Gly Glu Val Gly Pro Ala Gly Ser Pro Gly Ser Asn Gly Ala
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Pro Gly Gln Arg Gly Glu Pro Gly Pro Gln Gly His Ala Gly Ala Gln
 850 855 860

Gly Pro Pro Gly Pro Pro Gly Ile Asn Gly Ser Pro Gly Gly Lys Gly
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Glu Met Gly Pro Ala Gly Ile Pro Gly Ala Pro Gly Leu Met Gly Ala
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Arg Gly Pro Pro Gly Pro Ala Gly Ala Asn Gly Ala Pro Gly Leu Arg
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Gly Gly Ala Gly Glu Pro Gly Lys Asn Gly Ala Lys Gly Glu Pro Gly
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Pro Arg Gly Glu Arg Gly Glu Ala Gly Ile Pro Gly Val Pro Gly Ala
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Lys Gly Glu Asp Gly Lys Asp Gly Ser Pro Gly Glu Pro Gly Ala Asn
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Gly Leu Pro Gly Ala Ala Gly Glu Arg Gly Ala Pro Gly Phe Arg Gly
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1835		1840		1845	
Ser Gln	Asn Ile Thr Tyr	His	Cys Lys Asn Ser	Ile	Ala Tyr Met
1850		1855		1860	
Asp Gln	Ala Ser Gly Asn Val	Lys Lys Ala Leu	Lys	Leu Met Gly	
1865		1870		1875	
Ser Asn	Glu Gly Glu Phe Lys	Ala Glu Gly Asn	Ser	Lys Phe Thr	
1880		1885		1890	
Tyr Thr	Val Leu Glu Asp	Gly	Cys Thr Lys His	Thr	Gly Glu Trp
1895		1900		1905	
Ser Lys	Thr Val Phe Glu Tyr	Arg Thr Arg Lys	Ala	Val Arg Leu	
1910		1915		1920	
Pro Ile	Val Asp Ile Ala	Pro	Tyr Asp Ile Gly	Gly	Pro Asp Gln
1925		1930		1935	
Glu Phe	Gly Val Asp Val	Gly	Pro Val Cys Phe	Leu	
1940		1945		1950	

<210> 11
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide for PCR

<400> 11
 gcttccagtc ttccgagcat gccaaaataa tagtggg

37

<210> 12

<211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide for PCR

<400> 12
 cccactatta ttttgcatg ctcggaagac tggaagc 37

<210> 13
 <211> 4815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA molecule based on procollagen type III N-propeptide.
 Sequence prior to N100 replaced with the sequence for the G3
 domain of the alpha3 chain of laminin-5 whilst retaining the
 collagen III signal sequence.

<400> 13
 atgatgagct ttgtgcaaaa ggggagctgg ctacttctcg ctctgcttca tcccactatt 60
 attttgcat gctcggaaga ctggaagctt gtgcgatctg cctcattctc cagaggagga 120
 caattgagtt tctactgattt gggcttacca cctactgacc acctccaggc ctcatttgga 180
 tttcagacct ttcaaccag tggcatatta ttagatcatc agacatggac aaggaacctg 240
 caggtcactc tggaagatgg ttacattgaa ttgagcacca gcgatagcgg cggcccaatt 300
 tttaaatctc cacagacgta tatggatggg ttactgcatt atgtatctgt aataagcgac 360
 aactctggac tacgggttct catcgatgac cagcttctga gaaatagcaa aaggctaaaa 420
 cacatttcaa gttcccggca gtctctgcgt ctgggcggga gcaattttga gggttgtatt 480
 agcaatgttt ttgtccagag gttatcactg agtcctgaag tcctagattt gaccagtaac 540
 tctctcaaga gagatgtgtc cctgggaggc tgcagttaa acaaaccacc ttttctaattg 600
 ttgcttaaag gttctaccag gtttaacaag accaagactt ttcgtatcaa ccagctgttg 660
 caggacacac cagtggcctc cccaaggagc gtgaagggtg ggcaagatgc taatgggtcaa 720
 ggacctcaag gcccgaagg agatccaggc cctcctggta ttcctgggag aaatgggtgac 780
 cctgggtattc caggacaacc aggggtcccct ggttctcctg gccccctgg aatctgtgaa 840
 tcatgcccta ctggctctca gaactattct cccagtatg attcatatga tgtcaagtct 900
 ggagtagcag taggaggact cgcaggctat cctggaccag ctggcccccc aggccctccc 960
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cctggtgaac ctgggcaagc tggtccttca ggccctccag gacctcctgg tgctataggt	1080
ccatctgggtc ctgctggaaa agatggagaa tcaggtagac ccggacgacc tggagagcga	1140
ggattgcctg gacctccagg tatcaaaggt ccagctggga tacctggatt ccctgggatg	1200
aaaggacaca gaggcttcga tggacgaaat ggagaaaagg gtgaaacagg tgctcctgga	1260
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 gaatggagca aaacagtctt tgaatatcga acacgcaagg ctgtgagact acctattgta 4740
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 gtttgctttt tataa 4815

<210> 14
 <211> 1604
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Sequence of modified pro-alpha chain.

 <400> 14

Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu
 1 5 10 15

His Pro Thr Ile Ile Leu Ala Cys Ser Glu Asp Trp Lys Leu Val Arg
 20 25 30

Ser Ala Ser Phe Ser Arg Gly Gly Gln Leu Ser Phe Thr Asp Leu Gly
 35 40 45

Leu Pro Pro Thr Asp His Leu Gln Ala Ser Phe Gly Phe Gln Thr Phe
 50 55 60

Gln Pro Ser Gly Ile Leu Leu Asp His Gln Thr Trp Thr Arg Asn Leu
 65 70 75 80

Gln Val Thr Leu Glu Asp Gly Tyr Ile Glu Leu Ser Thr Ser Asp Ser
 85 90 95

Gly Gly Pro Ile Phe Lys Ser Pro Gln Thr Tyr Met Asp Gly Leu Leu
 100 105 110

His Tyr Val Ser Val Ile Ser Asp Asn Ser Gly Leu Arg Leu Leu Ile
 115 120 125

Asp Asp Gln Leu Leu Arg Asn Ser Lys Arg Leu Lys His Ile Ser Ser
 130 135 140

Ser Arg Gln Ser Leu Arg Leu Gly Gly Ser Asn Phe Glu Gly Cys Ile
 145 150 155 160

Ser Asn Val Phe Val Gln Arg Leu Ser Leu Ser Pro Glu Val Leu Asp
 165 170 175

Leu Thr Ser Asn Ser Leu Lys Arg Asp Val Ser Leu Gly Gly Cys Ser
 180 185 190

Leu Asn Lys Pro Pro Phe Leu Met Leu Leu Lys Gly Ser Thr Arg Phe
 195 200 205

Asn Lys Thr Lys Thr Phe Arg Ile Asn Gln Leu Leu Gln Asp Thr Pro
 210 215 220

Val Ala Ser Pro Arg Ser Val Lys Val Trp Gln Asp Ala Asn Gly Gln
 225 230 235 240

Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly
 245 250 255

Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln Pro Gly Ser Pro Gly Ser
 260 265 270

Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn
 275 280 285

Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val Lys Ser Gly Val Ala Val
 290 295 300

Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala Gly Pro Pro Gly Pro Pro
 305 310 315 320

Gly Pro Pro Gly Thr Ser Gly His Pro Gly Ser Pro Gly Ser Pro Gly
 325 330 335

Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln Ala Gly Pro Ser Gly Pro
 340 345 350

Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser Gly Pro Ala Gly Lys Asp

355

360

365

Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly Glu Arg Gly Leu Pro Gly
 370 375 380

Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile Pro Gly Phe Pro Gly Met
 385 390 395 400

Lys Gly His Arg Gly Phe Asp Gly Arg Asn Gly Glu Lys Gly Glu Thr
 405 410 415

Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly Leu Pro Gly Glu Asn Gly
 420 425 430

Ala Pro Gly Pro Met Gly Pro Arg Gly Ala Pro Gly Glu Arg Gly Arg
 435 440 445

Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Ala Arg
 450 455 460

Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly Pro Pro Gly Thr Ala Gly
 465 470 475 480

Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu Val Gly Pro Ala Gly Ser
 485 490 495

Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg Gly Glu Pro Gly Pro Gln
 500 505 510

Gly His Ala Gly Ala Gln Gly Pro Pro Gly Pro Pro Gly Ile Asn Gly
 515 520 525

Ser Pro Gly Gly Lys Gly Glu Met Gly Pro Ala Gly Ile Pro Gly Ala
 530 535 540

Pro Gly Leu Met Gly Ala Arg Gly Pro Pro Gly Pro Ala Gly Ala Asn
 545 550 555 560

Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Glu Pro Gly Lys Asn Gly
 565 570 575

Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu Arg Gly Glu Ala Gly Ile
 580 585 590

Pro Gly Val Pro Gly Ala Lys Gly Glu Asp Gly Lys Asp Gly Ser Pro
 595 600 605

Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly Ala Ala Gly Glu Arg Gly
 610 615 620

Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro Asn Gly Ile Pro Gly Glu
 625 630 635 640

Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro Gly Pro Ala Gly Pro Arg
 645 650 655

Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly Val Pro Gly Gly Pro Gly
 660 665 670

Met Arg Gly Met Pro Gly Ser Pro Gly Gly Pro Gly Ser Asp Gly Lys
 675 680 685

Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser Gly Arg Pro Gly Pro Pro
 690 695 700

Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly Val Met Gly Phe Pro Gly
 705 710 715 720

Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys Asn Gly Glu Arg Gly Gly
 725 730 735

Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro Gly Lys Asn Gly Glu Thr
 740 745 750

Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly Pro Gly Gly Asp Lys Gly
 755 760 765

Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu Gln Gly Leu Pro Gly Thr
 770 775 780

Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro Gly Glu Pro Gly Pro Lys
 785 790 795 800

Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Gly Lys Gly Asp Ala Gly
 805 810 815

Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu Ala Gly Ala Pro Gly Leu
 820 825 830

Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu Gly Gly Lys Gly Ala Ala
 835 840 845

Gly Pro Pro Gly Pro Pro Gly Ala Ala Gly Thr Pro Gly Leu Gln Gly
 850 855 860

Met Pro Gly Glu Arg Gly Gly Leu Gly Ser Pro Gly Pro Lys Gly Asp
 865 870 875 880

Lys Gly Glu Pro Gly Gly Pro Gly Ala Asp Gly Val Pro Gly Lys Asp
 885 890 895

Gly Pro Arg Gly Pro Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly
 900 905 910

Gln Pro Gly Asp Lys Gly Glu Gly Gly Ala Pro Gly Leu Pro Gly Ile
 915 920 925

Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Thr Gly Pro Pro
 930 935 940

Gly Pro Ala Gly Phe Pro Gly Ala Pro Gly Gln Asn Gly Glu Pro Gly
 945 950 955 960

Gly Lys Gly Glu Arg Gly Ala Pro Gly Glu Lys Gly Glu Gly Gly Pro
 965 970 975

Pro Gly Val Ala Gly Pro Pro Gly Gly Ser Gly Pro Ala Gly Pro Pro
 980 985 990

Gly Pro Gln Gly Val Lys Gly Glu Arg Gly Ser Pro Gly Gly Pro Gly
 995 1000 1005

Ala Ala Gly Phe Pro Gly Ala Arg Gly Leu Pro Gly Pro Pro Gly
 1010 1015 1020

Ser Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser Gly Ser Pro Gly
 1025 1030 1035

Lys Asp Gly Pro Pro Gly Pro Ala Gly Asn Thr Gly Ala Pro Gly
 1040 1045 1050

Ser Pro Gly Val Ser Gly Pro Lys Gly Asp Ala Gly Gln Pro Gly
 1055 1060 1065

Glu Lys Gly Ser Pro Gly Ala Gln Gly Pro Pro Gly Ala Pro Gly
 1070 1075 1080

Pro Leu Gly Ile Ala Gly Ile Thr Gly Ala Arg Gly Leu Ala Gly
 1085 1090 1095

Pro Pro Gly Met Pro Gly Pro Arg Gly Ser Pro Gly Pro Gln Gly
 1100 1105 1110

Val Lys Gly Glu Ser Gly Lys Pro Gly Ala Asn Gly Leu Ser Gly
 1115 1120 1125

Glu Arg Gly Pro Pro Gly Pro Gln Gly Leu Pro Gly Leu Ala Gly
 1130 1135 1140

Thr Ala Gly Glu Pro Gly Arg Asp Gly Asn Pro Gly Ser Asp Gly
 1145 1150 1155

Leu Pro Gly Arg Asp Gly Ser Pro Gly Gly Lys Gly Asp Arg Gly
 1160 1165 1170

Glu Asn Gly Ser Pro Gly Ala Pro Gly Ala Pro Gly His Pro Gly
 1175 1180 1185

Pro Pro Gly Pro Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly
 1190 1195 1200

Glu Ser Gly Pro Ala Gly Pro Ala Gly Ala Pro Gly Pro Ala Gly
 1205 1210 1215

Ser Arg Gly Ala Pro Gly Pro Gln Gly Pro Arg Gly Asp Lys Gly
 1220 1225 1230

Glu Thr Gly Glu Arg Gly Ala Ala Gly Ile Lys Gly His Arg Gly
 1235 1240 1245

Phe Pro Gly Asn Pro Gly Ala Pro Gly Ser Pro Gly Pro Ala Gly

1250		1255		1260
Gln Gln Gly Ala Ile Gly Ser	Pro Gly Pro Ala Gly	Pro Arg Gly		
1265	1270	1275		
Pro Val Gly Pro Ser Gly Pro	Pro Gly Lys Asp Gly	Thr Ser Gly		
1280	1285	1290		
His Pro Gly Pro Ile Gly Pro	Pro Gly Pro Arg Gly	Asn Arg Gly		
1295	1300	1305		
Glu Arg Gly Ser Glu Gly Ser	Pro Gly His Pro Gly	Gln Pro Gly		
1310	1315	1320		
Pro Pro Gly Pro Pro Gly Ala	Pro Gly Pro Cys Cys	Gly Gly Val		
1325	1330	1335		
Gly Ala Ala Ala Ile Ala Gly	Ile Gly Gly Glu Lys	Ala Gly Gly		
1340	1345	1350		
Phe Ala Pro Tyr Tyr Gly Asp	Glu Pro Met Asp Phe	Lys Ile Asn		
1355	1360	1365		
Thr Asp Glu Ile Met Thr Ser	Leu Lys Ser Val Asn	Gly Gln Ile		
1370	1375	1380		
Glu Ser Leu Ile Ser Pro Asp	Gly Ser Arg Lys Asn	Pro Ala Arg		
1385	1390	1395		
Asn Cys Arg Asp Leu Lys Phe	Cys His Pro Glu Leu	Lys Ser Gly		
1400	1405	1410		
Glu Tyr Trp Val Asp Pro Asn	Gln Gly Cys Lys Leu	Asp Ala Ile		
1415	1420	1425		
Lys Val Phe Cys Asn Met Glu	Thr Gly Glu Thr Cys	Ile Ser Ala		
1430	1435	1440		
Asn Pro Leu Asn Val Pro Arg	Lys His Trp Trp Thr	Asp Ser Ser		
1445	1450	1455		
Ala Glu Lys Lys His Val Trp	Phe Gly Glu Ser Met	Asp Gly Gly		
1460	1465	1470		

Phe Gln Phe Ser Tyr Gly Asn Pro Glu Leu Pro Glu Asp Val Leu
1475 1480 1485

Asp Val Gln Leu Ala Phe Leu Arg Leu Leu Ser Ser Arg Ala Ser
1490 1495 1500

Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp
1505 1510 1515

Gln Ala Ser Gly Asn Val Lys Lys Ala Leu Lys Leu Met Gly Ser
1520 1525 1530

Asn Glu Gly Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe Thr Tyr
1535 1540 1545

Thr Val Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp Ser
1550 1555 1560

Lys Thr Val Phe Glu Tyr Arg Thr Arg Lys Ala Val Arg Leu Pro
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Ile Val Asp Ile Ala Pro Tyr Asp Ile Gly Gly Pro Asp Gln Glu
1580 1585 1590

Phe Gly Val Asp Val Gly Pro Val Cys Phe Leu
1595 1600

<210> 15
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
cttgtagatg cggccgcatg aagtcacg gcctctt

37

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

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<223> PCR primer	
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gtaatacgac tcactatagg gc	22
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<211> 18	
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 <223> PCR primer

 <400> 21
 agaggcttcg atggacga 18

 <210> 22
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 <223> PCR primer

 <400> 22
 ggactgcgag gtggtgca 18

 <210> 23
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 <400> 23
 ttctcccagg aataccag 18

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 <223> PCR primer

 <400> 24
 agggaatccg gcagttcc 18

 <210> 25
 <211> 18
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 <220>
 <223> PCR primer

 <400> 25
 ctcggggacc agatggcc 18

 <210> 26

<211> 4719
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA molecule based on procollagen type III N-propeptide.
 Procollagen type III N-propeptide sequence replaced with the
 sequence for SLPI whilst retaining the collagen III signal
 sequence.

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 gcccagtgcc ttagatacaa gaaacctgag tgccagagtg actggcagtg tccagggag 180
 aagagatgtt gtctgacac ttgtggcatc aaatgcctgg atcctgttga caccctaaac 240
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 cccaaccag aaattccatt tggagaatgt tgtgcagttt gccacagcc tccaactgct 600
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 cctggcccc ctggaatctg tgaatcatgc cctactggtc ctcagaacta ttctccccag 780
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 gggatacctg gattccctgg tatgaaagga cacagaggct tcgatggacg aaatggagaa 1140
 aagggtgaaa caggtgctcc tggattaaag ggtgaaaatg gtcttccagg cgaaaatgga 1200
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ggacacgctg	gtgctcaagg	tcctcctggc	cctcctggga	ttaatggtag	tcctgggtgg	1500
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gaatttggtg tggacgttgg ccctgtttgc tttttataa 4719

<210> 27

<211> 1572
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence of modified pro-alpha chain.

<400> 27

Met Lys Ser Ser Gly Leu Phe Pro Phe Leu Val Leu Leu Ala Leu Gly
1 5 10 15

Thr Leu Ala Pro Trp Ala Val Glu Gly Ser Gly Lys Ser Phe Lys Ala
20 25 30

Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys
35 40 45

Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys
50 55 60

Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn
65 70 75 80

Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys
85 90 95

Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys
100 105 110

Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser
115 120 125

Pro Val Lys Ala Ala Val Glu Gly Gly Cys Ser His Leu Gly Gln Ser
130 135 140

Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Gln Ile Cys Val
145 150 155 160

Cys Asp Ser Gly Ser Val Leu Cys Asp Asp Ile Ile Cys Asp Asp Gln
165 170 175

Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro Phe Gly Glu Cys Cys Ala
180 185 190

Val Cys Pro Gln Pro Pro Thr Ala Pro Thr Arg Pro Pro Asn Gly Gln
 195 200 205

Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly
 210 215 220

Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln Pro Gly Ser Pro Gly Ser
 225 230 235 240

Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn
 245 250 255

Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val Lys Ser Gly Val Ala Val
 260 265 270

Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala Gly Pro Pro Gly Pro Pro
 275 280 285

Gly Pro Pro Gly Thr Ser Gly His Pro Gly Ser Pro Gly Ser Pro Gly
 290 295 300

Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln Ala Gly Pro Ser Gly Pro
 305 310 315 320

Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser Gly Pro Ala Gly Lys Asp
 325 330 335

Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly Glu Arg Gly Leu Pro Gly
 340 345 350

Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile Pro Gly Phe Pro Gly Met
 355 360 365

Lys Gly His Arg Gly Phe Asp Gly Arg Asn Gly Glu Lys Gly Glu Thr
 370 375 380

Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly Leu Pro Gly Glu Asn Gly
 385 390 395 400

Ala Pro Gly Pro Met Gly Pro Arg Gly Ala Pro Gly Glu Arg Gly Arg
 405 410 415

Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Ala Arg

420

425

430

Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly Pro Pro Gly Thr Ala Gly
 435 440 445

Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu Val Gly Pro Ala Gly Ser
 450 455 460

Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg Gly Glu Pro Gly Pro Gln
 465 470 475 480

Gly His Ala Gly Ala Gln Gly Pro Pro Gly Pro Pro Gly Ile Asn Gly
 485 490 495

Ser Pro Gly Gly Lys Gly Glu Met Gly Pro Ala Gly Ile Pro Gly Ala
 500 505 510

Pro Gly Leu Met Gly Ala Arg Gly Pro Pro Gly Pro Ala Gly Ala Asn
 515 520 525

Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Glu Pro Gly Lys Asn Gly
 530 535 540

Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu Arg Gly Glu Ala Gly Ile
 545 550 555 560

Pro Gly Val Pro Gly Ala Lys Gly Glu Asp Gly Lys Asp Gly Ser Pro
 565 570 575

Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly Ala Ala Gly Glu Arg Gly
 580 585 590

Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro Asn Gly Ile Pro Gly Glu
 595 600 605

Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro Gly Pro Ala Gly Pro Arg
 610 615 620

Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly Val Pro Gly Gly Pro Gly
 625 630 635 640

Met Arg Gly Met Pro Gly Ser Pro Gly Gly Pro Gly Ser Asp Gly Lys
 645 650 655

Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser Gly Arg Pro Gly Pro Pro
 660 665 670

Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly Val Met Gly Phe Pro Gly
 675 680 685

Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys Asn Gly Glu Arg Gly Gly
 690 695 700

Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro Gly Lys Asn Gly Glu Thr
 705 710 715 720

Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly Pro Gly Gly Asp Lys Gly
 725 730 735

Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu Gln Gly Leu Pro Gly Thr
 740 745 750

Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro Gly Glu Pro Gly Pro Lys
 755 760 765

Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Gly Lys Gly Asp Ala Gly
 770 775 780

Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu Ala Gly Ala Pro Gly Leu
 785 790 795 800

Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu Gly Gly Lys Gly Ala Ala
 805 810 815

Gly Pro Pro Gly Pro Pro Gly Ala Ala Gly Thr Pro Gly Leu Gln Gly
 820 825 830

Met Pro Gly Glu Arg Gly Gly Leu Gly Ser Pro Gly Pro Lys Gly Asp
 835 840 845

Lys Gly Glu Pro Gly Gly Pro Gly Ala Asp Gly Val Pro Gly Lys Asp
 850 855 860

Gly Pro Arg Gly Pro Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly
 865 870 875 880

Gln Pro Gly Asp Lys Gly Glu Gly Gly Ala Pro Gly Leu Pro Gly Ile
 885 890 895

Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Thr Gly Pro Pro
 900 905 910

Gly Pro Ala Gly Phe Pro Gly Ala Pro Gly Gln Asn Gly Glu Pro Gly
 915 920 925

Gly Lys Gly Glu Arg Gly Ala Pro Gly Glu Lys Gly Glu Gly Gly Pro
 930 935 940

Pro Gly Val Ala Gly Pro Pro Gly Gly Ser Gly Pro Ala Gly Pro Pro
 945 950 955 960

Gly Pro Gln Gly Val Lys Gly Glu Arg Gly Ser Pro Gly Gly Pro Gly
 965 970 975

Ala Ala Gly Phe Pro Gly Ala Arg Gly Leu Pro Gly Pro Pro Gly Ser
 980 985 990

Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser Gly Ser Pro Gly Lys Asp
 995 1000 1005

Gly Pro Pro Gly Pro Ala Gly Asn Thr Gly Ala Pro Gly Ser Pro
 1010 1015 1020

Gly Val Ser Gly Pro Lys Gly Asp Ala Gly Gln Pro Gly Glu Lys
 1025 1030 1035

Gly Ser Pro Gly Ala Gln Gly Pro Pro Gly Ala Pro Gly Pro Leu
 1040 1045 1050

Gly Ile Ala Gly Ile Thr Gly Ala Arg Gly Leu Ala Gly Pro Pro
 1055 1060 1065

Gly Met Pro Gly Pro Arg Gly Ser Pro Gly Pro Gln Gly Val Lys
 1070 1075 1080

Gly Glu Ser Gly Lys Pro Gly Ala Asn Gly Leu Ser Gly Glu Arg
 1085 1090 1095

Gly Pro	Pro Gly	Pro Gln	Gly	Leu Pro	Gly Leu	Ala	Gly Thr	Ala
1100			1105			1110		
Gly Glu	Pro Gly	Arg Asp	Gly	Asn Pro	Gly Ser	Asp	Gly Leu	Pro
1115			1120			1125		
Gly Arg	Asp Gly	Ser Pro	Gly	Gly Lys	Gly Asp	Arg	Gly Glu	Asn
1130			1135			1140		
Gly Ser	Pro Gly	Ala Pro	Gly	Ala Pro	Gly His	Pro	Gly Pro	Pro
1145			1150			1155		
Gly Pro	Val Gly	Pro Ala	Gly	Lys Ser	Gly Asp	Arg	Gly Glu	Ser
1160			1165			1170		
Gly Pro	Ala Gly	Pro Ala	Gly	Ala Pro	Gly Pro	Ala	Gly Ser	Arg
1175			1180			1185		
Gly Ala	Pro Gly	Pro Gln	Gly	Pro Arg	Gly Asp	Lys	Gly Glu	Thr
1190			1195			1200		
Gly Glu	Arg Gly	Ala Ala	Gly	Ile Lys	Gly His	Arg	Gly Phe	Pro
1205			1210			1215		
Gly Asn	Pro Gly	Ala Pro	Gly	Ser Pro	Gly Pro	Ala	Gly Gln	Gln
1220			1225			1230		
Gly Ala	Ile Gly	Ser Pro	Gly	Pro Ala	Gly Pro	Arg	Gly Pro	Val
1235			1240			1245		
Gly Pro	Ser Gly	Pro Pro	Gly	Lys Asp	Gly Thr	Ser	Gly His	Pro
1250			1255			1260		
Gly Pro	Ile Gly	Pro Pro	Gly	Pro Arg	Gly Asn	Arg	Gly Glu	Arg
1265			1270			1275		
Gly Ser	Glu Gly	Ser Pro	Gly	His Pro	Gly Gln	Pro	Gly Pro	Pro
1280			1285			1290		
Gly Pro	Pro Gly	Ala Pro	Gly	Pro Cys	Cys Gly	Gly	Val Gly	Ala
1295			1300			1305		
Ala Ala	Ile Ala	Gly Ile	Gly	Gly Glu	Lys Ala	Gly	Gly Phe	Ala

1310		1315		1320
Pro Tyr Tyr Gly Asp Glu Pro Met Asp Phe Lys Ile Asn Thr Asp				
1325		1330		1335
Glu Ile Met Thr Ser Leu Lys Ser Val Asn Gly Gln Ile Glu Ser				
1340		1345		1350
Leu Ile Ser Pro Asp Gly Ser Arg Lys Asn Pro Ala Arg Asn Cys				
1355		1360		1365
Arg Asp Leu Lys Phe Cys His Pro Glu Leu Lys Ser Gly Glu Tyr				
1370		1375		1380
Trp Val Asp Pro Asn Gln Gly Cys Lys Leu Asp Ala Ile Lys Val				
1385		1390		1395
Phe Cys Asn Met Glu Thr Gly Glu Thr Cys Ile Ser Ala Asn Pro				
1400		1405		1410
Leu Asn Val Pro Arg Lys His Trp Trp Thr Asp Ser Ser Ala Glu				
1415		1420		1425
Lys Lys His Val Trp Phe Gly Glu Ser Met Asp Gly Gly Phe Gln				
1430		1435		1440
Phe Ser Tyr Gly Asn Pro Glu Leu Pro Glu Asp Val Leu Asp Val				
1445		1450		1455
Gln Leu Ala Phe Leu Arg Leu Leu Ser Ser Arg Ala Ser Gln Asn				
1460		1465		1470
Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp Gln Ala				
1475		1480		1485
Ser Gly Asn Val Lys Lys Ala Leu Lys Leu Met Gly Ser Asn Glu				
1490		1495		1500
Gly Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe Thr Tyr Thr Val				
1505		1510		1515
Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp Ser Lys Thr				
1520		1525		1530

Val Phe Glu Tyr Arg Thr Arg Lys Ala Val Arg Leu Pro Ile Val
 1535 1540 1545

Asp Ile Ala Pro Tyr Asp Ile Gly Gly Pro Asp Gln Glu Phe Gly
 1550 1555 1560

Val Asp Val Gly Pro Val Cys Phe Leu
 1565 1570

<210> 28
 <211> 11
 <212> PRT
 <213> Unknown

<220>
 <223> Sequence typically found in small leucine-rich proteoglycans.

<220>
 <221> MISC_FEATURE
 <222> (2)..(3)
 <223> X at polition 2 or 3 may be any amino acid.

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> X at polition 5 may be any amino acid.

<220>
 <221> MISC_FEATURE
 <222> (7)..(8)
 <223> X at polition 7 or 8 may be any amino acid.

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> X at polition 10 may be any amino acid.

<220>
 <221> MISC_FEATURE
 <222> (11)..(11)
 <223> X at polition 11 is selected from L and I only.

<400> 28

Leu Xaa Xaa Leu Xaa Leu Xaa Xaa Asn Xaa Xaa
 1 5 10